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January 22, 2003

CERTIFICATE OF MAILING
37 C.F.R 1.8

I hereby certify that this correspondence is being deposited with the U.S. Postal Service with sufficient postage as First Class Mail in an envelope addressed to: Commissioner for Patents, Washington, DC 20231, on the date below:

January 22, 2003 — Date
Gina N. Shishima

Commissioner for Patents
Washington, D.C. 20231

Re: *SN 10/029,397 entitled "METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS" by Murphy et al.*
Our ref: AMBI:076US/10106991

Commissioner:

Enclosed please find the following for filing in the above-referenced patent application:

(1) Response to Restriction Requirement Dated January 13, 2003; and

(2) A return postcard to acknowledge receipt of these materials. Please date stamp and mail this postcard.

Should any fees under 37 C.F.R. §§ 1.16 to 1.21 be required for any reason relating to the enclosed materials, the Commissioner is authorized to deduct said fees from Fulbright & Jaworski L.L.P. Account No.: 50-1212/AMBI:076US.

Very truly yours,

Gina N. Shishima
Reg. No. 45,104

GNS/lb
Enclosures

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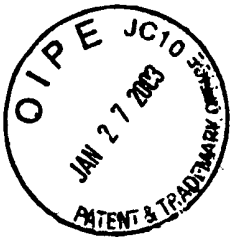

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Date

Gina N. Shishima

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:
Murphy et al.

Serial No.: 10/029,397

Filed: December 20, 2001

For: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS

Group Art Unit: 1634

Examiner: Chakrabarti, Arun K.

Atty. Dkt. No.: AMBI:076US

RESPONSE TO RESTRICTION REQUIREMENT
DATED JANUARY 13, 2003

Commissioner for Patents
Washington, D.C. 20231

Commissioner:

This paper is submitted in response to the Restriction Requirement dated January 13, 2003 for which the date for response is February 13, 2003. Therefore, this response is timely filed.

It is believed that no fee is due; however, should any fees under 37 C.F.R. §§ 1.16 to 1.21 be required for any reason relating to this document, the Commissioner is authorized to deduct said fees from Fulbright & Jaworski L.L.P. Account No.: 50-1212/AMBI:076US.

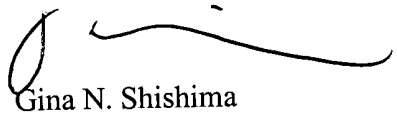
RESPONSE TO RESTRICTION REQUIREMENT

In response to the restriction requirement which the Examiner imposed, Applicants elect, without traverse, to prosecute claims 1-54 and 83-85, *i.e.*, the Group I claims. A copy of the elected claims is found in Appendix A for the Examiner's convenience.

Applicants also elect the species of SEQ ID NO:17. Claims 1, 2, and 3 are generic to claim 4, which recites SEQ ID NO:17. Applicants reserve the right, should allowable subject matter be found based on the elected species, to have a search on the broader genus be conducted. Applicants also assume they will be entitled to consideration of claims to additional species should a generic claim be found allowable.

The Examiner is invited to contact the undersigned attorney at (512) 536-3081 with any questions, comments or suggestions relating to the referenced patent application.

Respectfully submitted,



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Date: January 22, 2003

1. A method for depleting or isolating a targeted nucleic acid from a sample comprising:

a) incubating the sample with a first bridging oligonucleotide comprising (1) at least one bridging region comprising at least 5 nucleic acid residues and (2) at least one targeting region comprising at least 5 nucleic acid residues, under conditions allowing hybridization between the first targeting region and the targeted nucleic acid;

b) incubating the first bridging oligonucleotide with a capture oligonucleotide comprising a nonreacting structure and a capture region comprising at least 5 nucleic acid residues, under conditions allowing hybridization between the bridging region and the capture region; and

c) isolating the targeted nucleic acid from the remainder of the sample.

2. The method of claim 1 wherein the targeted nucleic acid is rRNA.

3. The method of claim 2, wherein the rRNA is prokaryotic 16S, prokaryotic 23S, eukaryotic 17S or 18S, or eukaryotic 28S rRNA.

4. The method of claim 3, wherein the rRNA comprises the sequence of SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:72, or SEQ ID NO:73.

5. The method of claim 1, wherein the sample comprises eukaryotic nucleic acid.

6. The method of claim 1, wherein the sample comprises prokaryotic nucleic acid.

7. The method of claim 6, wherein the prokaryotic nucleic acid is from a gram positive bacterium.

8. The method of claim 6, wherein the prokaryotic nucleic acid is from a gram negative bacterium.

9. The method of claim 1, wherein the bridging region, targeting region, or capture region comprises at least 10 nucleic acid residues.

10. The method of claim 9, wherein the bridging region, targeting region, or capture region comprises at least 15 nucleic acid residues.

11. The method of claim 10, wherein the bridging region, targeting region, or capture region comprises at least 20 nucleic acid residues.

12. The method of claim 1, wherein the bridging region or the capture region is polypurine or polypyrimidine.

13. The method of claim 12, wherein the bridging region is polypurine and the capture region is polypyrimidine.

14. The method of claim 1, further comprising incubating the sample with a second bridging oligonucleotide comprising (1) at least one bridging region comprising at least 5 nucleic acid residues and (2) at least one targeting region comprising at least 5 nucleic acid residues, under conditions allowing hybridization between the targeting region of the second bridging oligonucleotide and the targeted nucleic acid.

15. The method of claim 14, wherein the targeting region of the first bridging oligonucleotide is complementary to the sequence of a targeted nucleic acid and the targeting region of the

second bridging oligonucleotide is complementary to a different sequence of a targeted nucleic acid.

16. The method of claim 15, wherein the targeting region of the first bridging oligonucleotide and the targeting region of the second bridging oligonucleotide are complementary to the same targeted nucleic acid.

17. The method of claim 15, wherein the targeting region of the first bridging oligonucleotide and the targeting region of the second bridging oligonucleotide are complementary to different targeted nucleic acids.

18. The method of claim 17, wherein the targeting region of the first bridging oligonucleotide is complementary to a sequence of the largest rRNA molecule and the targeting region of the second bridging oligonucleotide is complementary to a sequence of the second largest rRNA molecule in the sample.

19. The method of claim 14, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 100 and 5000 residues of the 5' or 3' end of the targeted nucleic acid.

20. The method of claim 19, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 150 and 4000 residues of the 5' or 3' end of the targeted nucleic acid.

21. The method of claim 20, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 200 and 3000 residues of the 5' or 3' end of the targeted nucleic acid.

22. The method of claim 21, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 250 and 2000 residues of the 5' or 3' end of the targeted nucleic acid.

23. The method of claim 22, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 300 and 1500 residues of the 5' or 3' end of the targeted nucleic acid.

24. The method of claim 23, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 350 and 1000 residues of the 5' or 3' end of the targeted nucleic acid.

25. The method of claim 24, wherein targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 400 and 900 residues of the 5' or 3' end of the targeted nucleic acid.

26. The method of claim 25, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 450 and 800 residues of the 5' or 3' end of the targeted nucleic acid.

27. The method of claim 26, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence located between 500 and 700 residues of the 5' or 3' end of the targeted nucleic acid.

28. The method of claim 14, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence at the 3' or 5' end of the targeted nucleic acid.

29. The method of claim 14, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence not within 100 residues from the 3'or 5' end of the targeted nucleic acid.

30. The method of claim 14, wherein targeting region of the first or second bridging oligonucleotide hybridizes to a sequence not within 200 residues from the 3'or 5' end of the targeted nucleic acid.

31. The method of claim 14, wherein the targeting region of the first or second bridging oligonucleotide hybridizes to a sequence not within 400 residues from the 3'or 5' ends of the targeted nucleic acid.

32. The method of claim 14, wherein the targeting region of the first or second bridging oligonucleotide comprises SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, or SEQ ID NO:22.

33. The method of claim 1, wherein the bridging oligonucleotide comprises a second targeting region comprising at least 5 nucleic acid residues complementary to a different sequence than the sequence to which the first targeting region is complementary.

34. The method of claim 33, wherein the first targeting region is complementary to a different targeting nucleic acid than the second targeting region is.

35. The method of claim 1, wherein the first bridging oligonucleotide comprises two bridging regions.

36. The method of claim 1, wherein the bridging oligonucleotide or the capture oligonucleotide is RNA, DNA, LNA, iso-bases, or a peptide nucleic acid.

37. The method of claim 1, further comprising washing the capture oligonucleotide after incubation with the sample and the bridging oligonucleotide.

38. The method of claim 1, wherein a) and b) are performed at the same temperature.

39. The method of claim 1, wherein a) and b) are performed at a different temperature.

40. The method of claim 38, wherein a) and b) are performed at the same time.

41. The method of claim 1, wherein the nonreacting structure comprises a bead comprising plastic, glass, teflon, silica, a magnet, cellulose, latex, polystyrene, nylon, cellulose, nitrocellulose, polymethacrylate, polyvinylchloride, or styrene-divinylbenzene

42. The method of claim 41, wherein isolating the targeted nucleic acid away from the sample comprises exposing the sample with the capture oligonucleotide to a magnetic field.

43. The method of claim 1, wherein the nonreacting structure is cellulose.

44. The method of claim 1, wherein the nonreacting structure is biotin.

45. The method of claim 44, wherein isolating the targeted nucleic acid comprises incubating the sample with streptavidin or avidin.

46. The method of claim 1, wherein the sample, capture oligonucleotide, and bridging oligonucleotide are incubated in a buffer comprising TMAC or TEAC.

47. The method of claim 1, further comprising:

d) discarding the portion of the sample that hybridizes to the capture oligonucleotide.

48. The method of claim 2, further comprising:

d) discarding the targeted rRNA nucleic acid; and

e) producing cDNA using mRNA in the remainder of the sample.

49. The method of claim 48, further comprising:

f) attaching the cDNA to a solid support, wherein a nucleic acid array is created.

50. The method of claim 49, wherein the solid support is plastic, glass, or nylon.

51. The method of claim 50, wherein the solid support is a plate.

52. The method of claim 51, wherein the plate is a multiple-well plate.

53. The method of claim 48, further comprising:

f) contacting a nucleic acid array with the cDNA.

54. A method for depleting rRNA from a sample comprising:

a) incubating the sample with at least a first (1) bridging oligonucleotide comprising a bridging region comprising a poly-purine region of at least 5 residues and a targeting region comprising at least 5 contiguous nucleic acid residues complementary to a sequence of an rRNA molecule and a (2) capture oligonucleotide comprising a magnetic bead and a capture region comprising a poly-pyrimidine region of at least 5 residues, under conditions to allow hybridization between the bridging oligonucleotide and the capture oligonucleotide and the bridging oligonucleotide and the rRNA;

b) incubating the sample with a magnetic bead; and

c) isolating the magnetic bead.

83. A method for depleting or isolating a targeted rRNA from a sample comprising:

a) obtaining the kit of claim 55;

b) incubating the sample with the bridging oligonucleotide under conditions allowing hybridization between the targeting region and the targeted rRNA;

c) incubating the bridging oligonucleotide with the capture oligonucleotide under conditions allowing hybridization between the bridging region and the capture region; and

d) isolating the targeted rRNA from the remainder of the sample by incubating the sample with a magnetic field.

84. The method of claim 83, further comprising:

e) obtaining the remainder of the sample enriched for mRNA;

f) preparing cDNA from the mRNA.

85. The method of claim 84, further comprising:

g) constructing a nucleic acid array with the cDNA.